

# Package ‘SCLCBam’

April 12, 2018

**Type** Package

**Title** Sequence data from chromosome 4 of a small-cell lung tumor

**Version** 1.10.0

**Date** 2015-02-18

**Author** Thomas Kuilman

**Maintainer** Thomas Kuilman <t.kuilman@nki.nl>

**Depends** R(>= 2.10)

**Suggests** BiocStyle

**Description** Whole-exome sequencing data from a murine small-cell lung tumor; only contains data of chromosome 4.

**License** GPL-2

**biocViews** SequencingData, LungCancerData

**NeedsCompilation** no

## R topics documented:

getPathBamFolder . . . . . 1

**Index** 3

---

getPathBamFolder	<i>SCLCBam: Sequence data from chromosome 4 of a small-cell lung tumor</i>
------------------	--

---

## Description

Sequence reads from chromosome 4 of a whole-exome sequencing approach on a small-cell lung tumor.

## Usage

```
getPathBamFolder()
```

## Details

The `getPathBamFolder()` function returns the full path name to the folder containing the `.bam` file.

**Value**

Returns the full path name of the folder containing the .bam file.

**Author(s)**

Thomas Kuilman (t.kuilman@nki.nl)

**References**

The dataset was downloaded from the European Nucleotide Archive using the accession number PRJEB6954 using sample accession number SAMEA2697779, and reads on chromosome 4 were extracted. The full .bam file containing data for all chromosomes can be downloaded from here <http://www.ebi.ac.uk/ena/data/view/SAMEA2697779>

**Examples**

```
getPathBamFolder()
```

# Index

`getPathBamFolder`, [1](#)

`SCLCBam (getPathBamFolder)`, [1](#)